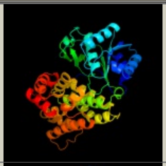
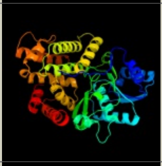
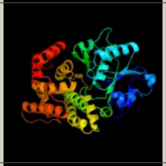
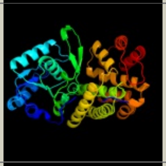
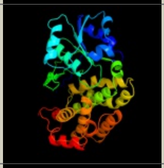
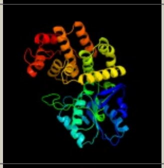
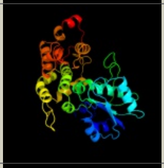
Email	l.a.kelley@imperial.ac.uk
Description	P0A9S1
Date	Wed Jan 25 15:20:20 GMT 2012
Unique Job ID	ad8e95e8ad4da78b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bfjK_	Alignment		100.0	44	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
2	d1rrma_	Alignment		100.0	97	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
3	c3ox4D_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
4	d1vlja_	Alignment		100.0	25	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
5	d1oj7a_	Alignment		100.0	23	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
6	d1o2da_	Alignment		100.0	25	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
7	c3hl0B_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
8	c3iv7B_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alcohol dehydrogenase iv; **PDBTitle:** crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
9	c3jzdA_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
10	c3rf7A_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
11	d1jq5a_	Alignment		100.0	22	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase

12	c1ta9A_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
13	d1kq3a_	Alignment		100.0	24	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
14	c3uhjE_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
15	c3ce9A_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
16	c3okfA_	Alignment		100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
17	c1xahA_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of staphlyococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+
18	d1sg6a_	Alignment		100.0	14	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
19	c2gruB_	Alignment		100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-deoxy-scyllo-inosose synthase; **PDBTitle:** crystal structure of 2-deoxy-scyllo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
20	c3clhA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of 3-dehydroquinate synthase (dhqs)from2 helicobacter pylori
21	d1ujna_	Alignment	not modelled	100.0	19	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
22	c3orsD_	Alignment	not modelled	97.1	13	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
23	d1qcza_	Alignment	not modelled	97.1	16	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
24	d1o4va_	Alignment	not modelled	97.0	18	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
25	c3rggD_	Alignment	not modelled	97.0	19	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
26	d1u11a_	Alignment	not modelled	97.0	13	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
27	c2fw9A_	Alignment	not modelled	97.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole

						ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
28	c3lp6D_	Alignment	not modelled	96.9	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
29	d2jgra1	Alignment	not modelled	96.8	12	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
30	d2p1ra1	Alignment	not modelled	96.8	16	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
31	d2bona1	Alignment	not modelled	96.7	12	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
32	d1xmpa_	Alignment	not modelled	96.6	17	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
33	c3trhI_	Alignment	not modelled	96.6	16	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
34	c2bonB_	Alignment	not modelled	96.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipid kinase; **PDBTitle:** structure of an escherichia coli lipid kinase (yegs)
35	c2h31A_	Alignment	not modelled	96.3	13	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
36	d1u0ta_	Alignment	not modelled	96.1	24	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
37	d1qo0a_	Alignment	not modelled	95.5	9	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
38	c2qv7A_	Alignment	not modelled	95.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase dgkb; **PDBTitle:** crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
39	c3s40C_	Alignment	not modelled	95.2	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
40	c2ywxA_	Alignment	not modelled	95.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
41	d2qv7a1	Alignment	not modelled	94.7	22	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
42	d1pfka_	Alignment	not modelled	92.8	18	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
43	c3pfnB_	Alignment	not modelled	92.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
44	c3snrA_	Alignment	not modelled	92.4	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
45	c1zxxA_	Alignment	not modelled	92.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
46	d1ewka_	Alignment	not modelled	92.1	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
47	c2j37W_	Alignment	not modelled	91.5	21	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
48	d4pfka_	Alignment	not modelled	91.5	21	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
49	c2an1D_	Alignment	not modelled	91.4	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
50	c3sg0A_	Alignment	not modelled	91.3	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
51	c3q41B_	Alignment	not modelled	91.3	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1; **PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd)
52	c3mdqA_	Alignment	not modelled	91.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of an exopolyphosphatase (chu_0316)

						from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
53	c3i09A_	Alignment	not modelled	91.0	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic branched-chain amino acid-binding protein; **PDBTitle:** crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
54	c3hi0B_	Alignment	not modelled	90.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
55	c2iy3A_	Alignment	not modelled	90.8	11	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
56	c3i45A_	Alignment	not modelled	90.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of putative twin-arginine translocation pathway2 signal protein from rhodospirillum rubrum atcc 11170
57	d2f48a1	Alignment	not modelled	90.6	17	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
58	c3n0wA_	Alignment	not modelled	90.3	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc branched chain amino acid family transporter, **PDBTitle:** crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bxe_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
59	c1t6dB_	Alignment	not modelled	89.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
60	c3eafA_	Alignment	not modelled	89.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
61	d2ji7a1	Alignment	not modelled	89.8	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
62	c3opyH_	Alignment	not modelled	89.7	21	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
63	c3opyB_	Alignment	not modelled	89.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
64	c3rfqC_	Alignment	not modelled	89.0	20	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
65	d1ovma1	Alignment	not modelled	88.9	22	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
66	c3dm5A_	Alignment	not modelled	88.9	24	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
67	c2dwcB_	Alignment	not modelled	88.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
68	c3lopA_	Alignment	not modelled	88.5	8	**PDB header:**substrate binding protein **Chain:** A: **PDB Molecule:**substrate binding periplasmic protein; **PDBTitle:** crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
69	c1kjjA_	Alignment	not modelled	88.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
70	c3k2qA_	Alignment	not modelled	87.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
71	d1v4va_	Alignment	not modelled	87.6	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
72	c1qzwC_	Alignment	not modelled	87.5	22	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
73	d1xi8a3	Alignment	not modelled	87.4	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
74	c2e4wA_	Alignment	not modelled	87.4	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**metabotropic glutamate receptor 3; **PDBTitle:** crystal structure of the extracellular region of the group ii2 metabotropic glutamate receptor complexed with 1s,3s-acpd
75	c2j289_	Alignment	not modelled	87.3	16	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54;

						PDBTitle: model of e. coli srp bound to 70s rncs
76	c2i2aA_	Alignment	not modelled	87.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
77	c2higA_	Alignment	not modelled	87.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
78	c2floA_	Alignment	not modelled	87.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
79	c3tqrA_	Alignment	not modelled	87.0	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
80	d1zpda1	Alignment	not modelled	86.9	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
81	c3h5lB_	Alignment	not modelled	86.6	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative branched-chain amino acid abc **PDBTitle:** crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
82	c3o8oB_	Alignment	not modelled	86.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase subunit beta; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
83	c3hutA_	Alignment	not modelled	86.4	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative branched-chain amino acid abc **PDBTitle:** crystal structure of a putative branched-chain amino acid2 abc transporter from rhodospirillum rubrum
84	c3cf4G_	Alignment	not modelled	86.2	14	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
85	d1vh3a_	Alignment	not modelled	86.0	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
86	c3opyE_	Alignment	not modelled	85.7	23	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
87	d2ihta1	Alignment	not modelled	85.6	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
88	c2q5cA_	Alignment	not modelled	85.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
89	d2ez9a1	Alignment	not modelled	85.5	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
90	c3cerD_	Alignment	not modelled	85.5	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**possible exopolyphosphatase-like protein; **PDBTitle:** crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
91	c3kg2A_	Alignment	not modelled	85.4	10	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
92	d1zl0a2	Alignment	not modelled	84.5	9	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
93	d1pvda1	Alignment	not modelled	84.4	25	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
94	c3lkbB_	Alignment	not modelled	84.0	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**probable branched-chain amino acid abc **PDBTitle:** crystal structure of a branched chain amino acid abc2 transporter from thermus thermophilus with bound valine
95	d1t9ba1	Alignment	not modelled	84.0	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
96	c3t0nA_	Alignment	not modelled	83.6	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal; **PDBTitle:** crystal structure of twin-arginine translocation pathway signal from2 rhodopseudomonas palustris bisb5
97	c1zrsB_	Alignment	not modelled	83.4	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
98	c3dcjA_	Alignment	not modelled	83.1	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
99	d2auna2	Alignment	not modelled	82.8	9	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
100	d1q6za1	Alignment	not modelled	82.5	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain

						Family: Pyruvate oxidase and decarboxylase, middle domain
101	c2xecD_	Alignment	not modelled	82.1	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
102	c2g4rB_	Alignment	not modelled	81.9	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
103	c3opyG_	Alignment	not modelled	81.8	18	**PDB header:**transferase **Chain:** G: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
104	d1y5ea1	Alignment	not modelled	81.5	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
105	d2pjua1	Alignment	not modelled	81.4	11	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
106	c3ip5A_	Alignment	not modelled	81.1	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein (amino acid); **PDBTitle:** structure of atu2422-gaba receptor in complex with alanine
107	c2pjkA_	Alignment	not modelled	80.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
108	c3o8oC_	Alignment	not modelled	80.3	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
109	c1m6vE_	Alignment	not modelled	79.9	13	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
110	c3dnfB_	Alignment	not modelled	79.8	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
111	c3o8nA_	Alignment	not modelled	79.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
112	c2ywrA_	Alignment	not modelled	79.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
113	c3jpyA_	Alignment	not modelled	79.2	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glutamate [nmda] receptor subunit epsilon-2; **PDBTitle:** crystal structure of the zinc-bound amino terminal domain of the nmda2 receptor subunit nr2b
114	d1a9xa4	Alignment	not modelled	79.1	12	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
115	c2is8A_	Alignment	not modelled	79.1	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
116	c3p9xB_	Alignment	not modelled	79.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
117	c2yhsA_	Alignment	not modelled	79.0	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
118	c2jkzB_	Alignment	not modelled	78.6	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
119	d2g2ca1	Alignment	not modelled	78.6	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
120	d1mkza_	Alignment	not modelled	78.3	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like